

REMARKS

This Amendment is being submitted in response to the Official Action dated 24 March 2006, the deadline for response being 24 June 2006. The title and specification have been amended to correct informalities. Claims 1 and 2 have been amended, and they remain pending in this application.

The Examiner objected to the title and specification for a number of informalities, all of which have been corrected herein. The Examiner indicated that trademarked terms, such as BLAST™, should be capitalized and accompanied by the generic terminology. Applicant has amended the specification accordingly, and no new matter is intended by the Applicant. Additionally to facilitate prosecution, Applicant renumbered the specification pages (in the first instance, page 3 was misnumbered as page 2 and consequently, each subsequent page was misnumbered).

The Examiner rejected claims 1 and 2 under 35 U.S.C. §101 as being directed to non-statutory subject matter. Particularly, the Examiner contends that “[t]here is no stated outcome to the claimed method of handling a database for bioinformatics such that a concrete, tangible, and useful result is apparent.” The Applicant respectfully disagrees. The claimed method is essentially a process for querying a bioinformatics database by collecting a plurality of user requests for comparison in a queue and then comparing each bioinformatics database entry one-by-one to all user requests in the queue. When any single user request has been fully compared to all the database entries it is removed from the queue, and the process continues iteratively for all remaining user requests. This approach greatly expedites the server time needed to handle all of the plural user requests when compared to the prior art approach of

devoting all server resources to handling each user requests one-by-one, and comparing each successively to all database entries. Thus, the method “performs *time and cost-effective modeling of biological networks*” because database sequence data is simultaneously collected and analyzed to all queued requests (page 13 (renumbered), lines 5-11). This result/outcome of the claimed method is concrete, tangible, and useful. A concrete result is one that is “substantially repeatable”. *In re Swartz*, 232 F. 3d 862, 864, 56 USPQ2d 1703, 1704 (Fed. Cir. 2000). Every time the method claimed in claims 1 and 2 is performed, the result is the same: *time-and cost-effective modeling of biological networks*. Thus, the method produces a concrete result. A tangible result is a “real-word result”. *Benson*, 409 U.S. at 71-72, 175 USPQ at 676-77 (invention ineligible because had “no substantial practical application”). Here the result: *time-and cost-effective modeling of biological networks* has “substantial practical application” because it allows for *more efficient* gene sequencing. Gene sequencing is more efficient because the server accesses the bioinformatics database only once to handle all user requests (page 14 (renumbered), lines 3-4). As the Examiner indicated a “useful” result must satisfy the utility requirement of section 101. Claims 1 and 2 are demonstrated, *infra*, to have utility under section 101. Applicant does not think the Examiner contends that no speedier method of querying a database can possibly be statutory subject matter under 35 USC 101, and will therefore refrain from a diatribe of other patents and case law that support the opposite. Rather, Applicant believes that the Examiner’s rejection stemmed mainly from indefinite claims, and hence claims 1 and 2 are fully amended to concretely recite the discrete steps in the method as well as the concrete result. Therefore, claim 1 and likewise depending claim 2 as amended are directed to statutory subject matter.

The Examiner further rejected claims 1 and 2 under 35 U.S.C. §101 as lacking utility.

The Examiner asserts that “[t]he method of handling a database for bioinformatics is not supported by a specific asserted utility because the specification does not set forth a specific asserted utility nor is a well-established utility found in the art. The method storing sequence information related to bioinformatics without knowing the significance of that sequence information or the relationship of the sequence information does not equate to a specific or substantial utility.” Applicant respectfully disagrees. It is well known that the very purpose of handling a bioinformatics database (such as FASTA™ or BLAST™) is to compare the sequence information of the *query* with the sequence information of the *library* to determine if there is any relationship between the two. If there is a relationship between the *query* and *library* sequences (i.e. they are similar), then this relationship is analyzed to determine the protein functions and relations between species. It is known that “[p]rediction of protein-coding genes in newly sequenced [i.e. library] DNA is very important in large-scale genome sequencing projects.” See Rogozin et al., Gene structure prediction using information on homologous protein sequence, Oxford University Press, Vol. 12, no. 3, 1996, page 161. Thus, because the claimed invention simultaneously collects and analyzes sequence-variation data, this allows for time-and cost-effective modeling of large-scale, complex genome sequencing projects and thereby provides significant utility. Because this utility is well established in the art, claims 1 and 2 have utility.

The Examiner further rejected claims 1 and 2 under 35 U.S.C. §112, first paragraph for not enabling one skilled in the art to use the invention. The Examiner asserts that the claimed invention lacks utility and thus one skilled in the art would not know how to use the claimed invention. Applicant demonstrated that the utility for claims 1 and 2 is well established in the art, *supra*, pg. 3, and claims 1 and 2 are herein amended in light of 112 first paragraph to concretely recite the steps of the method in such fashion to allow one skilled in the art to use the

invention. Since Examiner equated enablement to utility here, and further because utility for claims 1 and 2 is demonstrated *supra*, ergo claims 1 and 2 are enabling as well.

The Examiner further rejected claims 1 and 2 under 35 U.S.C. §112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter, which the applicant regards as his invention. Particularly, the Examiner states that claim 1 lacks antecedent basis for “each user terminal” and “the current order”, and that “comparison” is unclear. Applicant has amended claim 1 to introduce “a plurality of user terminals”. Also, the “current order” is deleted and claim 1 has been amended to introduce the bioinformatics database as storing a “*plurality of gene sequences*”. Claim 1 is further amended to delete “comparison” from the preamble, and rather it is reflected properly in gerund form (-ing) in the step of “*comparing one of the plurality of gene sequences stored in the bioinformatics database with all of the requests stored in said queue inclusive of said new request and said earlier requests*” (see also page 6 (renumbered), line 6-8). Claim 1 has been further amended to clarify the method by introducing each step with a word in gerund form, to place the claim proper format. Depending claim 2 has been amended for clarity as well. No new matter was added, nor was such the intent of the Applicant.

The Examiner further rejected claims 1 and 2 under 35 U.S.C. §102 (b) as being anticipated by Eckman et al. (Bioinformatics (1998) Vol. 14, No. 1, pages 2-13). Eckman et al. discloses the Merck Gene Index (MGI) browser, which is a World Wide Web-based system for mining the MGI and related genomic data (see p. 2 of Eckman et al.). Additionally, the MGI browser integrates data (including expressed sequence tag (EST) sequence data) from a variety of sources and storage formats. However the Eckman et al. method does not query a bioinformatics database by collecting a plurality of user requests for comparison in a queue and

then comparing each bioinformatics database entry one-by-one to all user requests in the queue, nor does he remove a request from the queue when that user request has been fully compared to all the database entries, iteratively, for all remaining user requests, as does the method claimed in claims 1 and likewise depending claim 2. Specifically, Eckman et al. do not check whether there are previous requests for comparison of gene sequences earlier stored in said queue, and when said checking step determines that there are previous requests for comparison of gene sequences earlier stored in said queue, comparing one of the plurality of gene sequences stored in the bioinformatics database with all of the requests stored in said queue inclusive of said new request and said earlier requests, identifying any of the requests stored in said queue inclusive of said new request and said earlier requests that have been fully compared with all sequences stored in the bioinformatics database, and removing any of the identified fully compared requests. These are essential limitations of claim 1 and 2 that are not taught or suggested by Eckman et al. Considering these remarks, it is respectfully submitted that the Eckman et al. reference fails to anticipate amended claim 1, and likewise depending amended claim 2. Therefore, it is believed that the amended claims 1 and 2 are patentably distinguished from the Eckman et al. reference and are therefore allowable.

Additionally, the Examiner rejected claims 1 and 2 under 35 U.S.C. §102 (b) as being anticipated by Li et al. (*Bioinformatics* (2000) Vol. 16, No. 12, pages 1105-1110). The Examiner contends that Li teaches a multiple intermediate sequence search method (MISS) consisting of initial search, selection of intermediate queries, intermediate search loop, and final result analysis. However, the MISS method disclosed in Li does not run database searches of multiple queries simultaneously. Rather, the MISS method in Li specifically discloses: running a database search with the first query, *selecting new queries from the first search's output and,*

Application of: Kim, et al.

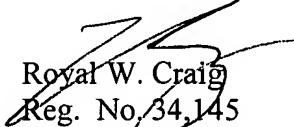
Appln. No. 10/668,026

Page 14

after validation, used in subsequent searches, and then repeating the procedure as long as new sequences are found. Thus, the method disclosed in Li, which utilizes then first search's output to select new queries, is entirely different than the method claimed in claims 1 and 2, which allows users to select sequences (i.e. make queries to database) independently of each other. Claim 1 indicates that multiple queries are run simultaneously ("checking whether there are subsequent searches in the queue, wherein said step of checking whether there are subsequent searches in the queue is performed simultaneously with said step of receiving a first gene sequence from a user terminal to store it in a queue; comparing sequences stored in the bioinformatics database with first and subsequent searches in the queue....") Therefore, it is respectfully submitted that amended claim 1 and likewise amended dependent claim 2 do not anticipate Li et al. (Bioinformatics (2000) Vol. 16, No. 12, pages 1105-1110). Consequently amended claims 1 and 2 are patentably distinguished.

In view of the above, pending claims 1 and 2 are believed to avoid all the objections/rejections set forth in the Official Action. The case should be in allowance. A Notice to this effect is respectfully requested, and the Examiner is invited to call the undersigned at (410) 419-6899 to discuss any remaining issues.

Respectfully submitted,


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